

SEQUENCE LISTING

| 5 | SEQ ID NO: 1 is a mouse 312C2 nucleic acid sequence. SEQ ID NO: 2 is a mouse 312C2 amino acid sequence. SEQ ID NO: 3 is a human 312C2 nucleic acid sequence. SEQ ID NO: 4 is a human 312C2 amino acid sequence. SEQ ID NO: 5 is a reverse translation sequence. SEQ ID NO: 6 is clone A8 amino acid sequence. SEQ ID NO: 7 is clone A5 amino acid sequence. |
|---|---|
| 10 | SEQ ID NO: 8 is clone G10 amino acid sequence. |
| 15 | (1) GENERAL INFORMATION: (i) APPLICANT: Gorman, Daniel M. Randall, Troy D. Zlotnik, Albert |
| | (ii) TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED REAGENTS |
| 20 | (iii) NUMBER OF SEQUENCES: 8 |
| 1 mil | <pre>(iv) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: DNAX Research Institute (B) STREET: 901 California Avenue (C) CITY: Palo Alto (D) STATE: California (E) COUNTRY: USA (F) ZIP: 94304-1104</pre> |
| \] 30 [[] | (v) COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk |
| a 113 113 113 113 113 113 113 113 113 11 | (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 |
| 40 | (vi) CURRENT APPLICATION DATA:(A) APPLICATION NUMBER: US 08/911,423(B) FILING DATE: 14-AUG-1997(C) CLASSIFICATION: |
| 45 | <pre>(vii) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: US 60/023,419 (B) FILING DATE: 16-AUG-1996</pre> |
| | <pre>(vii) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: US 60/027,901 (B) FILING DATE: 07-OCT-1996</pre> |
| 50 | <pre>(viii) ATTORNEY/AGENT INFORMATION: (A) NAME: Ching, Edwin P. (B) REGISTRATION NUMBER: 34,090 (C) REFERENCE/DOCKET NUMBER: DX0612K</pre> |
| 55 | (ix) TELECOMMUNICATION INFORMATION: (A) TELEPHONE: 650-852-9196 (B) TELEFAX: 650-496-1200 |



| 12) INFORMATION FOR DEC 15 NO.1 | (2) | INFORMATION | FOR | SEO | ID | NO:1: |
|---------------------------------|-----|-------------|-----|-----|----|-------|
|---------------------------------|-----|-------------|-----|-----|----|-------|

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1073 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear |
|----|--|
| 10 | (ii) MOLECULE TYPE: cDNA |

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(ix) FEATURE:

15

(A) NAME/KEY: CDS
(B) LOCATION: 68..751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| 20 CTCGAGATCC ATTGTCTGG AAAGGGAACT CCTGAAATCA GCCGACAGAA GACTCAGGAG AAGCACT ATG GGG GCA TGG GCC ATG CTG TAT GGA GTC TCG ATG CTC TGT Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys 1 | | | | | | | | (X1) SEQUENCE DESCRIPTION: SEQ ID NO.1. | | | | | | | | | | | | | |
|--|-----|------------|------------|------------|------------|------------|------------|---|------------|------------|-----------------|------------|------------|------------|------------|------------|------------|------------|--|--|--|
| Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys 10 | 60 | AGGAG | ACTO | SAA C | ACAC | GCCG | ATCA | GAAA | r cci | BAACT | AAGGC | G A | GCTC | TTGT | CC A | SAGAT | CTCC | 20 | | | |
| GTG CTG GAC CTA GGT CAG CCG AGT GTA GTT GAG GAG CCT GGC TGT GGC Val Leu Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly 15 | 109 | TGT Cys | CTC Leu | ATG Met | TCG Ser | Val | GGA Gly | TAT Tyr | CTG Leu | ATG Met | GCC Ala 5 | TGG Trp | GCA Ala | GGG Gly | Met | CACT | AAGO | | | | |
| CTG TAT GCT CCA GGC AAG GAG GAC TGT CCA AAA GAA AGG TGC ATA TGT Leu Tyr Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys 50 GTC ACA CCT GAG TAC CAC TGT GGA GAC CCT CAG TGC AAG ATC TGC AAG Val Thr Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys 40 CAC TAC CCC TGC CAA CCA GGC CAG AGG GTG GAG TCT CAA GGG GAT ATT His Tyr Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile 80 45 GTG TTT GGC TTC CGG TGT GTT GCC TGT GCC ATG GGC ACC TTC TCC GCA Val Phe Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala 100 GGT CGT GAC GGT CAC TGC AGA CTT TGG ACC AAC TGT TCT CAG TTT GGA Gly Arg Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly 115 | 157 | Gly | TGT Cys | GGC Gly | CCT Pro | GAG Glu | Glu | GTT Val | GTA Val | AGT Ser | CCG Pro | Gln | GGT Gly | CTA Leu | GAC Asp | CTG Leu | Val | | | | |
| CTG TAT GCT CCA GGC AAG GAG GAC TGT CCA AAA GAA AGG TGC ATA TGT Leu Tyr Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys GTC ACA CCT GAG TAC CAC TGT GGA GAC CCT CAG TGC AAG ATC TGC AAG Val Thr Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys 40 CAC TAC CCC TGC CAA CCA GGC CAG AGG GTG GAG TCT CAA GGG GAT ATT His Tyr Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile 80 GTG TTT GGC TTC CGG TGT GTT GCC TGT GCC ATG GGC ACC TTC TCC GCA Val Phe Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala 100 GGT CGT GAC GGT CAC TGC AGA CTT TGG ACC AAC TGT TCT CAG TTT GGA Gly Arg Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly 115 | 205 | AGC Ser | Cys | TGC Cys | CGC Arg | ACT Thr | AAC Asn | Asn | GGC Gly | AGT Ser | GGA Gly | AAC Asn | Gln | GTT Val | AAG Lys | GGC Gly | CCT Pro | | | | |
| Val Thr Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys 40 CAC TAC CCC TGC CAA CCA GGC CAG AGG GTG GAG TCT CAA GGG GAT ATT His Tyr Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile 80 GTG TTT GGC TTC CGG TGT GTT GCC TGT GCC ATG GGC ACC TTC TCC GCA Val Phe Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala 95 GGT CGT GAC GGT CAC TGC AGA CTT TGG ACC AAC TGT TCT CAG TTT GGA Gly Arg Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly 115 120 125 | 253 | TGT Cys | ATA Ile | Cys | AGG Arg | GAA Glu | AAA Lys | CCA Pro | Cys | GAC Asp | GAG Glu | AAG Lys | GGC Gly | Pro | GCT Ala | TAT Tyr | CTG Leu | : C : x | | | |
| His Tyr Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile 80 85 90 45 GTG TTT GGC TTC CGG TGT GTT GCC TGT GCC ATG GGC ACC TTC TCC GCA Val Phe Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala 95 100 105 110 GGT CGT GAC GGT CAC TGC AGA CTT TGG ACC AAC TGT TCT CAG TTT GGA Gly Arg Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly 115 120 125 | 301 | AAG Lys | TGC Cys | ATC Ile | Lys | TGC Cys | CAG Gln | CCT Pro | GAC Asp | Gly | TGT Cys | CAC His | TAC Tyr | GAG Glu | Pro | ACA Thr | GTC Val | 40 | | | |
| GTG TTT GGC TTC CGG TGT GTT GCC TGT GCC ATG GGC ACC TTC TCC GCA Val Phe Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala 95 100 105 110 GGT CGT GAC GGT CAC TGC AGA CTT TGG ACC AAC TGT TCT CAG TTT GGA Gly Arg Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly 115 120 125 | 349 | ATT Ile | GAT Asp | GGG Gly | CAA Gln | Ser | GAG Glu | GTG Val | AGG Arg | CAG Gln | Gly | CCA Pro | CAA Gln | TGC Cys | CCC Pro | Tyr | CAC His | 45 | | | |
| Gly Arg Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly 115 120 125 | 397 | Ala | TCC Ser | TTC Phe | ACC Thr | GGC Gly | Met | GCC Ala | TGT Cys | GCC Ala | GTT Val | Cys | CGG Arg | TTC Phe | GGC Gly | TTT Phe | Val | 45 | | | |
| | 445 | GGA Gly | Phe | CAG Gln | TCT Ser | TGT Cys | AAC Asn | Thr | TGG Trp | CTT Leu | AGA Arg | TGC Cys | His | GGT Gly | GAC Asp | CGT Arg | GGT Gly | 50 | | | |
| TTT CTC ACC ATG TTC CCT GGG AAC AAG ACC CAC AAT GCT GTG TGC ATC 55 Phe Leu Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile 130 135 140 | 493 | ATC Ile | Cys | Val | GCT Ala | AAT Asn | CAC His | ACC Thr | Lys | AAC Asn | GGG Gly | CCT Pro | Phe | Met | ACC Thr | CTC Leu | TTT Phe | 55 | | | |



| _ | CCG GAG CCA CTG CCC ACT GAG CAA TAC GGC CAT TTG ACT GTC ATC TTC Pro Glu Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe 145 150 155 | 541 |
|-------------|---|------|
| 5 | CTG GTC ATG GCT GCA TGC ATT TTC TTC CTA ACC ACA GTC CAG CTC GGC Leu Val Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly 160 165 170 | 589 |
| 10 | CTG CAC ATA TGG CAG CTG AGG AGG CAA CAC ATG TGT CCC CGA GAG ACC Leu His Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr 175 180 185 190 | 637 |
| 15 | CAG CCA TTC GCG GAG GTG CAG TTG TCA GCT GAG GAT GCT TGC AGC TTC Gln Pro Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe 195 200 205 | 685 |
| 20 | CAG TTC CCT GAG GAG GAA CGC GGG GAG CAG ACA GAA GAA | 733 |
| | CTG GGG GGT CGG TGG CCA TGAGGCCTGG TCTTCCTCTG TGCCCCAAGC Leu Gly Gly Arg Trp Pro 225 | 781 |
| ## 43 ## | CAGACGCTAC AAGACTTGCC CAGCTATACC CTTGGTGAGA GCAGGGGCCA TGCTCTGCAC | 841 |
| 25 | CCTTCCCTGG GCCTGGCCCT GCTCCCCTCA ACAGTGGCGG AAGTGGGTGT ATGAGAGCGG | 901 |
| · 30 | TGAGTTACGA TTGGGCCCTA TGGCTGCCTT TCTCATTTGA CAGCTCTGTT GGAGTAGGGT | 961 |
| £ | CTTTGGGCCC ACCAAGAGCA CCACGTTTAG CACAAGATCT TGTACAAGAA TAAATACTTG | 1021 |
| 35 | TTTAGTAACC TGAAAAAAA AAAAAAAAGG GCGGCCGCGG AGGCCGAATT CC | 1073 |
| 11 35 [] | (2) INFORMATION FOR SEQ ID NO:2: | |
| 4 0 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 228 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear | |
| 45 | (ii) MOLECULE TYPE: protein | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: | |
| | Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys Val Leu 1 5 10 15 | |
| 50 | Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly Pro Gly 20 25 30 | |
| 55 | Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser Leu Tyr 35 40 45 | |
| | Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys Val Thr 50 55 60 | |



| | Pro 65 | Glu | Tyr | His | Cys | Gly 70 | Asp | Pro | Gln | Cys | Lys 75 | Ile | Cys | Lys | His | Tyr 80 | | |
|-----------------|-----------------|------------|------------|--------------|-----------------|-----------------------------|-------------|-------------|------------|------------------|------------|------------|------------|------------|------------------|------------|---|----|
| 5 | Pro | Сув | Gln | Pro | Gly 85 | Gln | Arg | Val | Glu | Ser 90 | Gln | Gly | Asp | Ile | Val 95 | Phe | | |
| 10 | Gly | Phe | Arg | Cys 100 | Val | Ala | Cys | Ala | Met 105 | Gly | Thr | Phe | Ser | Ala 110 | Gly | Arg | | |
| 10 | Asp | Gly | His 115 | Cys | Arg | Leu | Trp | Thr 120 | Asn | Cys | Ser | Gln | Phe 125 | Gly | Phe | Leu | | • |
| 15 | Thr | Met 130 | Phe | Pro | Gly | Asn | Lys 135 | Thr | His | Asn | Ala | Val 140 | Cys | Ile | Pro | Glu | | |
| | Pro 145 | Leu | Pro | Thr | Glu | Gln 150 | Tyr | Gly | His | Leu | Thr 155 | Val | Ile | Phe | Leu | Val 160 | | |
| 20 | Met | Ala | Ala | Cys | 11e 165 | Phe | Phe | Leu | Thr | Thr 170 | Val | Gln | Leu | Gly | Leu 175 | His | | |
|] 2 5 | Ile | Trp | Gln | Leu 180 | Arg | Arg | Gln | His | Met 185 | Cys | Pro | Arg | Glu | Thr 190 | Gln | Pro | | |
| # J | Phe | Ala | Glu 195 | Val | Gln | Leu | Ser | Ala 200 | Glu | Asp | Ala | Cys | Ser 205 | Phe | Gln | Phe | | |
| 30 | Pro | Glu 210 | Glu | Glu | Arg | Gly | Glu 215 | Gln | Thr | Glu | Glu | Lys 220 | Cys | His | Leu | Gly | | |
| 1 | Gly 225 | Arg | Trp | Pro | | | | | | | | | | ÷ | | | | |
| _35 | (2) | INF | ORMA | TION | FOR | SEQ | ID | NO:3 | : | | | | | | | | | |
| 40 | , . | (i | (| A) L B) T | ENGT YPE: | HARA H: 1 nuc DEDN | 006 leic | base aci | pai d | rs | | | | | | | | |
| 40 | | | | | | OGY: | | | 910 | | | | | | | | | |
| 45 | | (ii |) MO | LECU | LE T | YPE: | cDN | 'A | | | | | | | | | | |
| 45 | | (ix | (| | AME/ | KEY: | | | | | | | | | | | , | |
| 50 | | (xi |) SE | QUEN | CE D | ESCR | IPTI | ON: | SEQ | ÍD N | 0:3: | | | | | | | |
| 55 | ATG Met 1 | Ala | CAG Gln | CAC His | GGG Gly 5 | Ala | ATG Met | GGC Gly | GCG Ala | TTT Phe 10 | Arg | GCC Ala | CTG Leu | TGC Cys | GGC Gly 15 | CTG Leu | | 48 |



| | | GCG Ala | CTG Leu | CTG Leu | TGC Cys 20 | GCG Ala | CTC Leu | AGC Ser | CTG Leu | GGT Gly 25 | CAG Gln | CGC Arg | CCC Pro | ACC Thr | GGG Gly 30 | GGT Gly | CCC Pro | 96 |
|---|-----------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| | 5 | GGG Gly | TGC Cys | GGC Gly 35 | CCT Pro | GGG Gly | CGC Arg | CTC Leu | CTG Leu 40 | CTT Leu | GGG Gly | ACG Thr | GGA Gly | ACG Thr 45 | GAC Asp | GCG Ala | CGC Arg | 144 |
| | 10 | TGC Cys | TGC Cys 50 | CGG Arg | GTT Val | CAC His | ACG Thr | ACG Thr 55 | CGC Arg | TGC Cys | TGC Cys | CGC Arg | GAT Asp 60 | TAC Tyr | CCG Pro | GGC Gly | GAG Glu | 192 |
| | 15 | GAG Glu 65 | TGC Cys | TGT Cys | TCC Ser | GAG Glu | TGG Trp 70 | GAC Asp | TGC Cys | ATG Met | TGT Cys | GTC Val 75 | CAG Gln | CCT Pro | GAA Glu | TTC Phe | CAC His 80 | 240 |
| | 20 | TGC Cys | GGA Gly | GAC Asp | CCT Pro | TGC Cys 85 | TGC Cys | ACG Thr | ACC Thr | TGC Cys | CGG Arg 90 | CAC His | CAC His | CCT Pro | TGT Cys | CCC Pro 95 | CCA Pro | 288 |
| | 25 | GGC Gly | CAG Gln | GGG Gly | GTA Val 100 | CAG Gln | TCC Ser | CAG Gln | GGG Gly | AAA Lys 105 | TTC Phe | AGT Ser | TTT Phe | GGC Gly | TTC Phe 110 | CAG Gln | TGT Cys | 336 |
| And the thing the | 25 | ATC Ile | GAC Asp | TGT Cys 115 | GCC Ala | TCG Ser | GGG Gly | ACC Thr | TTC Phe 120 | TCC Ser | GGG Gly | GGC Gly | CAC His | GAA Glu 125 | GGC Gly | CAC | TGC Cys | 384 |
| | 30 | AAA Lys | CCT Pro 130 | TGG Trp | ACA Thr | GAC Asp | TGC Cys | ACC Thr 135 | CAG Gln | TTC Phe | GGG Gly | TTT Phe | CTC Leu 140 | ACT Thr | GTG Val | TTC | CCT Pro | 432 |
| | 35 | GGG Gly 145 | AAC Asn | AAG Lys | ACC Thr | CAC His | AAC Asn 150 | GCT Ala | GTG Val | TGC Cys | GTC Val | CCA Pro 155 | GGG Gly | TCC Ser | CCG Pro | CCG Pro | GCA Ala 160 | 480 |
| 9 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 40 | GAG Glu | CCG Pro | CTT Leu | GGG Gly | TGG Trp 165 | CTG Leu | ACC Thr | GTC Val | GTC Val | CTC Leu 170 | CTG Leu | GCC Ala | GTG Val | GCC Ala | GCC Ala 175 | TGC Cys | 528 |
| | 4.5 | GTC Val | CTC Leu | CTC Leu | CTG Leu 180 | ACC Thr | TCG Ser | GCC Ala | CAG Gln | CTT Leu 185 | Gly | CTG Leu | CAC His | ATC Ile | TGG Trp 190 | CAG Gln | CTG Leu | 576 |
| | 45 | AGG Arg | AGT Ser | CAG Gln 195 | Cys | ATG Met | TGG Trp | CCC Pro | CGA Arg 200 | Glu | ACC Thr | CAG Gln | CTG Leu | CTG Leu 205 | Leu | GAG Glu | GTG Val | 624 |
| | 50 | CCG Pro | CCG Pro 210 | Ser | ACC Thr | GAA Glu | GAC Asp | GCC Ala 215 | Arg | AGC Ser | TGC Cys | CAG Gln | TTC Phe 220 | Pro | GAG Glu | GAA Glu | GAG Glu | 672 |
| | 55 | CGG Arg 225 | Gly | GAG Glu | CGA Arg | TCG Ser | GCA Ala 230 | Glu | GAG Glu | AAG Lys | GGG Gly | CGG Arg 235 | Leu | GGA Gly | GAC Asp | CTG Leu | TGG Trp 240 | 720 |

| | GORMAN | , et | al | • | | | | (| 68 | | | | | , | | DX(| 0612 | 2K |
|------------|---|------------|------------|-----------|-----------|------------|------------|------------|---------------|-----------|------------|------------|------------|-----------|-----------|------|------|-----|
| | GTG TGAG | CCT | GC (| CGTC | CTCC | GG G(| GCCA | CCGA | C CG | CAGC | CAGC | CCC | rccc | CAG | | | • | 773 |
| 5 | GAGCTCC | CCA (| GCCC | GCAGO | G G | CTCT | GCGT | r civ | CTC! | rggg | CCG | GCC | CTG (| CTCC | CCTGG | SC . | ; | 833 |
| | AGCAGAA | STG (| GTG | CAGG | AA GO | GTGG | CAGT | G AC | CAGC | ccc | TGG | ACCA' | rgc i | AGTT | CGGCG | G. | | 893 |
| 10 | CCGCTCT | AAA C | GATO | CCAAC | SC T | racg: | racgo | C GT | GCAT | GCGA | CGT | CATA | GCT (| CTTC | TATAC | T | 9 | 953 |
| | GTCACCT | AAA 1 | TCA | ATTC! | AC TY | GCC | GTCG' | r tr | raca <i>i</i> | ACGT | CCT | GACT | GGG 2 | AAA | | | 10 | 006 |
| 15 | (2) INFO | ORMAT | NOI | FOR | SEQ | ID I | NO:4 | · • | | | | | | | | | | |
| 20 | GTCACCTAAA TTCAATTCAC TGGCCGTCGT TTTACAACGT CCTGACTGGG AAA (2) INFORMATION FOR SEQ ID NO:4: (i) SEQUENCE CHARACTERISTICS: | | | | | | | | | | | | | | | | | |
| | (: | ii) N | OLEC | CULE | TYPI | E: pi | rote | in . | | | | | | | | | | |
| 25 | () | ki) S | SEQUE | ENCE | DESC | CRIP: | rion | : SEC | Q ID | NO: | 1: | | | | | | | |
| 4 5 | Met Ala 1 | Gln | His | Gly 5 | Ala | Met | Gly | Ala | Phe 10 | Arg | Ala | Leu | Cys | Gly 15 | Leu | | | |
| 30 | Ala Leu | Leu | Cys 20 | Ala | Leu | Ser | Leu | Gly 25 | Gln | Arg | Pro | Thr | Gly 30 | Gly | Pro | | | , |
| | Gly Cys | Gly 35 | Pro | Gly | Arg | Leu | Leu 40 | Leu | Gly | Thr | Gly | Thr 45 | Asp | Ala | Arg | | | |
| 35 | Cys Cys 50 | Arg | Val | His | Thr | Thr 55 | Arg | Cys | Cys | Arg | Asp 60 | Tyr | Pro | Gly | Glu | | | |
| 40 | Glu Cys 65 | Cys | Ser | Glu | Trp 70 | Asp | Cys | Met | Cys | Val 75 | Gln | Pro | Glu | Phe | His 80 | | | |
| 40 | Cys Gly | Asp | Pro | Cys 85 | Çys | Thr | Thr | Cys | Arg 90 | His | His | Pro | Cys | Pro 95 | Pro | | | |
| 45 | Gly Gln | Gly | Val 100 | Gln | Ser | Gln | Gly | Lys 105 | Phe | Ser | Phe | Gly | Phe 110 | Gln | Cys | | | |
| | Ile Asp | Cys 115 | Ala | Ser | Gly | Thr | Phe 120 | Ser | Gly | Gly | His | Glu 125 | Gly | His | Cys | | | |
| 50 | Lys Pro 130 | Trp | Thr | Asp | Cys | Thr 135 | Gln | Phe | Gly | Phe | Leu 140 | Thr | Val | Phe | Pro | | | |

Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala

Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys

| | Val Leu Leu Eur Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu 180 185 190 | | | | | | | | | | | | | | |
|------------|--|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|
| 5 | Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Glu Val 195 200 205 | | | | | | | | | | | | | | |
| | Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu 210 215 220 | | | | | | | | | | | | | | |
| 10 | Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp 225 230 235 240 | | | | | | | | | | | | | | |
| | Val | | | | | | | | | | | | | | |
| 15 | (2) INFORMATION FOR SEQ ID NO:5: | | | | | | | | | | | | | | |
| 20 | <pre>(2) INFORMATION FOR SEQ ID NO:5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 723 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:</pre> | | | | | | | | | | | | | | |
| 25 | , ——, | | | | | | | | | | | | | | |
| | ATGGCNCARC AYGGNGCNAT GGGNGCNTTY MGNGCNYTNT GYGGNYTNGC NYTNYTNTGY | 60 | | | | | | | | | | | | | |
| 30 | GCNYTNWSNY TNGGNCARMG NCCNACNGGN GGNCCNGGNT GYGGNCCNGG NMGNYTNYTN | 120 | | | | | | | | | | | | | |
| | YTNGGNACNG GNACNGAYGC NMGNTGYTGY MGNGTNCAYA CNACNMGNTG YTGYMGNGAY | 180 | | | | | | | | | | | | | |
| | TAYCCNGGNG ARGARTGYTG YWSNGARTGG GAYTGYATGT GYGTNCARCC NGARTTYCAY | 240 | | | | | | | | | | | | | |
| 35 | TGYGGNGAYC CNTGYTGYAC NACNTGYMGN CAYCAYCCNT GYCCNCCNGG NCARGGNGTN | 300 | | | | | | | | | | | | | |
| <i>:</i> | CARWSNCARG GNAARTTYWS NTTYGGNTTY CARTGYATHG AYTGYGCNWS NGGNACNTTY | 360 | | | | | | | | | | | | | |
| 40 | WSNGGNGGNC AYGARGGNCA YTGYAARCCN TGGACNGAYT GYACNCARTT YGGNTTYYTN | 420 | | | | | | | | | | | | | |
| | ACNGTNTTYC CNGGNAAYAA RACNCAYAAY GCNGTNTGYG TNCCNGGNWS NCCNCCNGCN | 480 | | | | | | | | | | | | | |
| 4.5 | GARCCNYTNG GNTGGYTNAC NGTNGTNYTN YTNGCNGTNG CNGCNTGYGT NYTNYTNYTN | 540 | | | | | | | | | | | | | |
| 45 | ACNWSNGCNC ARYTNGGNYT NCAYATHTGG CARYTNMGNW SNCARTGYAT GTGGCCNMGN | 600 | | | | | | | | | | | | | |
| | GARACNCARY TNYTNYTNGA RGTNCCNCCN WSNACNGARG AYGCNMGNWS NTGYCARTTY | 660 | | | | | | | | | | | | | |
| - 0 | CONCADO A DIVONOCANO A DIVONTUCANOCAN CADO ADA ADO CATACANVANTO MOAVVANTACO | 720 | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:6:

GTN

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids

(B) TYPE: amino acid



| | | | | | | SS: 8 linea | | le | | | | | | | | |
|-------------------|------------|------------|------------|------------|------------|----------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| 5 | (ii) | MOL | ECULI | E TYI | PE: 1 | pept: | ide | | | | | | | | | |
| 5 | (xi) | SEQ | JENCI | E DES | SCRII | OITS | 1: SI | EQ II | ON C | :6: | | | | | | • |
| 10 | Met 1 | Gly | Ala | Phe | Arg 5 | Ala | Leu | Cys | Gly | Leu 10 | Ala | Leu | Leu | Cys | Ala 15 | Leu |
| 10 | Ser | Leu | Gly | Gln 20 | Arg | Pro | Thr | Gly | Gly 25 | Pro | Gly | Cys | Gly | Pro 30. | Gly | Arg |
| 15 | Leu | Leu | Leu 35 | Gly | Thr | Gly | Thr | Asp 40 | Ala | Arg | Cys | Cys | Arg 45 | Val | His | Thr |
| | Thr | Arg 50 | Cys | Cys | Arg | Asp | Tyr 55 | Pro | Gly | Glu | Glu | Cys 60 | Cys | Ser | Glu | Trp |
| 20 | Asp 65 | Cys | Met | Cys | Va1 | Gln 70 | Pro | Glu | Phe | His | Cys 75 | Gly | Asp | Pro | Cys | Cys 80 |
| 1 1 1 25 | Thr | Thr | Cys | Arg | His 85 | His | Pro | Cys | Pro | Pro 90 | Gly | Gln | Gly | Val | Gln 95 | Ser |
| | Gln | Gly | Lys | Phe 100 | Ser | Phe | Gly | Phe | Gln 105 | Cys | Ile | Asp | Cys | Ala 110 | Ser | Gly |
| 30 | Thr | Phe | Ser 115 | Gly | Gly | His | Glu | Gly 120 | His | Cys | Lys | Pro | Trp 125 | Thr | Asp | Cys |
| | Thr | Gln 130 | Phe | Gly | Phe | Leu | Thr 135 | Val | Phe | Pro | Gly | Asn 140 | Lys | Thr | His | Asn |
| 35 | Ala 145 | Val | Cys | Val | Pro | Gly 150 | Ser | Pro | Pro | Ala | Glu 155 | Pro | Leu | Gly | Trp | Leu 160 |
| 40 | Thr | Val | Val | Leu | Leu 165 | Ala | Val | Ala | Ala | Cys 170 | Val | Leu | Leu | Leu | Thr 175 | Ser |
| | Ala | Gln | Leu | Gly 180 | Leu | His | Ile | Trp | Gln 185 | Leu | Arg | Lys | Thr | Gln 190 | Leu | Leu |
| 45 | Leu | Glu | Val 195 | Pro | Pro | Ser | Thr | Glu 200 | Asp | Ala | Arg | Ser | Cys 205 | Gln | Phe | Pro |

Glu Glu Glu Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly

215

50 Asp Leu Trp Val 225

210

(2) INFORMATION FOR SEQ ID NO:7:

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gly Ala Phe Arg Ala Leu Cys Gly Leu Ala Leu Leu Cys Ala Leu 1 5 10 15

10 Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro Gly Cys Gly Pro Gly Arg

Leu Leu Cly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr 35 40 45

Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu Glu Cys Cys Ser Glu Trp

Asp Cys Met Cys Val Gln Pro Glu Phe His Cys Gly Asp Pro Cys Cys 65 70 75 80

Thr Thr Cys Arg His His Pro Cys Pro Pro Gly Gln Gly Val Gln Ser 85 90 95

25 Gln Gly Lys Ser Trp Arg Cys Leu Trp Glu Ser Thr Gln Ala Arg Gly 100 105 110

Ser Thr Arg Ala Arg Gly Arg Ala Arg Gly His Arg Cys Pro Ala Arg 115 120 125

Thr Cys Gly Val Trp Gly Pro Glu Ser Cys Glu Ala Gly Gln Ala Arg 130 135 140

Pro Cys Ser Gly Thr Thr Gly His Glu Ala Leu Gly Val Ser Cys Pro 145 150 155 160

Cys Phe Leu Ser Leu Gly Phe Ser Ile Gln His Glu Gly Cys Glu Asn 165 170 175

Pro Ala Gly Arg Trp Gly Arg Val Pro Gly Ala Val Trp Leu Ser Gly
180 185 190

Pro Gly His Pro Ser Cys Leu Ser Ser Pro His Thr Glu Arg Ala Cys 195 200 205

Pro Val Pro Pro Gly Val Leu Ser Gly Ala Trp Gly Cys Thr Leu Phe 210 215 220

Trp Lys Glu Gln Leu Lys Ser Ser 50 225 230

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 311 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide

| _ | | | | | | | | | | | | | | | | |
|---------------|------------|------------|------------|------------|------------|------------|-------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| 5 | (xi) | SEQU | JENCE | E DES | CRI | OIT | 1: SI | EQ II | NO: | 8: | | - | | | | |
| 10 | Met 1 | Gly | Ala | Phe | Arg 5 | Ala | Leu | Cys | Gly | Leu 10 | Ala | Leu | Leu | Cys | Ala 15 | Leu |
| | Ser | Leu | Gly | Gln 20 | Arg | Pro | Thr | Gly | Gly 25 | Pro | Gly | Cys | Gly | Pro 30 | Gly | Arg |
| 15 | Leu | Leu | Leu 35 | Gly | Thr | Gly | Thr | Asp 40 | Ala | Arg | Cys | Cys | Arg 45 | Val | His | Thr |
| 20 | Thr | Arg 50 | Cys | Cys | Arg 、 | Asp | Tyr 55 | Pro | Gly | Glu | Glu | Cys 60 | Cys | Ser | Glu | Trp |
| 20 | Asp 65 | Cys | Met | Cys | Val | Gln 70 | Pro | Glu | Phe | His | Cys 75 | Gly | Asp | Pro | Cys | Cys 80 |
| 1 | Thr | Thr | Cys | Arg | His 85 | His | Pro | Cys | Pro | Pro 90 | Gly | Gln | Gly | Val | Gln 95 | Ser |
| And min in it | Gln | Gly | Lys | Phe 100 | Ser | Phe | Gly | Phe | Gln 105 | Cys | Ile | Asp | Cys | Ala 110 | Ser | Gly |
| 130 [[] | Thr | Phe | Ser 115 | Gly | Gly | His | Glu | Gly 120 | His | Cys | Lys | Pro | Trp 125 | Thr | Asp | Cys |
| 8.00 E | Thr | Gln 130 | Phe | Gly | Phe | Leu | Thr 135 | Val | Phe | Pro | Gly | Asn 140 | Lys | Thr | His | Asn |
| 135 1111 | Ala 145 | Val | Cys | Val | Pro | Gly 150 | Ser | Pro | Pro | Ala | Glu 155 | Pro | Leu | Gly | Trp | Leu 160 |
| 40 | Thr | Val | Val | Leu | Leu 165 | Ala | Val | Ala | Ala | Cys 170 | Val | Leu | Leu | Leu | Thr 175 | Ser |
| | Ala | Gln | Leu | Gly 180 | Leu | His | Ile | Trp | Gln 185 | Leu | Arg | Ser | Gln | Cys 190 | Met | Trp |
| 45 | Pro | Arg | Gly 195 | Leu | Ser | Gln | Pr ₍ 0 | Gly 200 | Ala | Gly | Arg | Trp | Glu 205 | His | Gly | Cys |
| 50 | Leu | Leu 210 | Thr | Val | Ala | Pro | Leu 215 | Gln | Arg | Pro | Ser | Cys 220 | Cys | Trp | Arg | Суѕ |
| 50 | Arg 225 | Arg | ,Arg | Pro | Lys | Thr 230 | Pro | Glu | Ala | Ala | Ser 235 | Ser | Pro | Arg | Lys | Ser 240 |
| 55 | Gly | Ala | Ser | Asp | Arg 245 | Gln | Arg | Arg | Arg | Gly 250 | Gly | Trp | Glu | Thr | Cys 255 | Gly |
| | Cys | Glu | Pro | Gly 260 | Arg | Pro | Pro | Gly | Pro 265 | Pro | Thr | Ala | Ala | Ser 270 | Pro | Ser |



| Pro | Gly | Ala | Pro | Gln | Ala | Ala | Gly | Ala | Leu | Arg | Ser | Ala | Leu | Gly | Arg |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | | 275 | | | | | 280 | | | | | 285 | | | |

Ala Leu Leu Pro Trp Gln Gln Lys Trp Val Gln Glu Gly Gly Ser Asp 290 295 300

Gln Arg Pro Gly Pro Cys Ser 305

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